Claims

1. A nucleic acid fragment comprising an inducible plant promoter, characterized in that said inducible promoter consists of the promoter of a plant class II O-methyltransferase (COMT II) gene.

2. The nucleic acid fragment as claimed in claim 1, characterized in that it consists of a plant COMT II promoter.

3. The nucleic acid fragment as claimed in either of claims 1 and 2, characterized in that the promoter is activated by injuries, viral infections, attacks from UV rays, chemical attacks or attacks by a pathogen, an insect or a nematode.

4. The nucleic acid fragment as claimed in one of claims 1 to 3, characterized in that the plant COMT II is a plant COMT which is not expressed in untreated healthy plants but which is expressed subsequent to a mechanical or chemical attack or an attack by a pathogen, an insect or a nematode.

5. The nucleic acid fragment as claimed in one of claims 1 to 4, characterized in that the plant is a monocotyledon plant or a dicotyledon plant in particular chosen from rice, wheat, barley, sunflower, maize, tobacco, rapeseed, soybean or *Arabidopsis thaliana*.

6. The nucleic acid fragment as claimed in claim 5, characterized in that the plant is a

dicotyledonous plant, preferably tobacco.

7. The nucleic acid fragment as claimed in one of claims 1 to 6, characterized in that the promoter comprises a sequence in 5′ of the translation initiation site, or start codon (ATG), of the coding sequence of the COMT II, which allows the transcription and the expression of said coding sequence.

8. The nucleic acid fragment as claimed in claim 1 to 7, characterized in that the promoter comprises a sequence of more than 600 nucleotides upstream of the COMT II ATG, preferably of more than 1 000 nucleotides upstream of the ATG, more preferentially of more than 1 200 nucleotides upstream of the ATG.

9. The nucleic acid fragment as claimed in one of claims 1 to 8, characterized in that the promoter comprises a transcription initiation site located less than 100 nucleotides upstream of the ATG, advantageously approximately 90 nucleotides upstream.

10. The nucleic acid fragment as claimed in one of claims 1 to 9, characterized in that the 3′ end of the promoter is located between the transcription initiation site and the ATG.

11. The nucleic acid fragment as claimed in claim 10, characterized in that the 3′ end of the promoter is located between 10 and 50 nucleotides downstream of the transcription initiation site, more

preferentially between 20 and 40 nucleotides downstream, even more preferentially between 20 and 30 nucleotides downstream.

12. The nucleic acid fragment as claimed in one of claims 1 to 11, characterized in that it consists of the tobacco COMT II promoter defined by the nucleotide sequence upstream of the ATG represented by sequence identifier 1 (SEQ ID NO 1), the sequences capable of hybridizing selectively to said sequence and the homologous sequences.

13. The nucleic acid fragment as claimed in claim 12, characterized in that it consists of the sequence between nucleotides 557 and 1796 of sequence identifier No. 1.

14. A chimeric gene (or expression cassette) which is functional in plant cells and the plants comprising, in the direction of transcription, a regulatory sequence in 5', a coding sequence and a regulatory sequence in 3', characterized in that the regulatory sequence in 5' comprises the nucleic acid fragment as claimed in one of claims 1 to 13.

15. The chimeric gene as claimed in claim 14, characterized in that the coding sequence comprises a coding sequence for a reporter gene or a coding sequence for a protein of interest.

16. The chimeric gene as claimed in claim 15, characterized in that the protein of interest

is a protein which confers on the plants properties of resistance to diseases or to insects.

17. The chimeric gene as claimed in claim 16, characterized in that the protein or peptide of interest is chosen from fungal elicitor peptides, in particular elicitins.

18. The chimeric gene as claimed in claim 17, characterized in that the fungal elicitor peptide is megaspermine.

19. The chimeric gene as claimed in claim 18, characterized in that megaspermine is represented by sequence indentifier No. 13 (SEQ ID 13).

20. The chimeric gene as claimed in claim 19, characterized in that it comprises the DNA sequence represented by sequence identifier No. 14 (SEQ ID 14).

21. A chimeric gene which is functional in plant cells and plants, characterized in that it comprises, in the direction of transcription, a regulatory sequence in 5' comprising an inducible promoter, a coding sequence for an elicitor and a regulatory sequence in 3'.

22. The chimeric gene as claimed in claim 21, characterized in that the elicitor is defined in claims 17 to 19.

23. The chimeric gene as claimed in either of claims 21 and 22, characterized in that the

inducible promoter is chosen from the promoters of phenylalanine ammonia lyase (PAL), of HMG-CoA reductase (HMG), of chitinases, of glucanases, of proteinase inhibitors (PIs), of PR1 family genes, of nopaline synthase (nos) or the vspB gene, the HMG2 promoter, the apple beta-galactosidase (ABG1) promoter or the apple aminocyclopropane carboxylate synthase (ACC synthase) promoter.

24. A cloning and/or expression vector for transforming plant cells or plants, characterized in that it contains at least one chimeric gene as claimed in claims 14 to 23.

25. A method for transforming plant cells, characterized in that it consists in integrating into the genome of said plant cells at least one chimeric gene as claimed in one of claims 14 to 23.

26. A transformed plant cell, characterized in that it comprises a chimeric gene as claimed in one of claims 14 to 23.

27. A transformed plant, characterized in that it comprises a chimeric gene as claimed in claims 14 to 23.

28. A plant, characterized in that it contains transformed cells as claimed in claim 26 or obtained using the method as claimed in claim 25.

29. The plant as claimed in claim 28, characterized in that it is regenerated from

transformed cells as claimed in claim 19 or obtained using the method as claimed in claim 18.

30. A plant derived from culturing and/or crossing regenerated plants as claimed in claim 29.

31. The plant as claimed in one of claims 27 to 30, characterized in that it is of the monocotyledon type, in particular a cereal, sugar cane, rice or maize, or of the dicotyledon type, in particular tobacco, soybean, rapeseed, cotton, sunflower, beetroot or clover.

32. A grain of plants as claimed in one of claims 27 to 31.